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; TOIG of: a29725 check: 7353 from: 1 to: 1014
; P1:A29725 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30), nuclear - human
; N:Alternate names: poly (ADP-ribose) polymerase; poly (ADP-ribose) synthetase;
; poly(ADP) polymerase
; C:Species: Homo sapiens (man)
; C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
; C:Accession: A29725; A28498; A39976; A26901; I38096; B33321; A35635;
; A61559; S14010
; R:Uchida, K.; Morita, T.; Sato, T.; Ogura, T.; Yamashita, R.; Noguchi, S.;
; Suzuki, H.; Nyunoya, H.; Miwa, M.; Sugimura, T.
; Biochem. Biophys. Res. Commun. 148, 617-622, 1987
; A:Title: Nucleotide sequence of a full-length cDNA for human fibroblast
; poly(ADP-ribose) polymerase.
; A:Reference number: A29725; MUID:88076933
; A:Accession: A29725
; A:Molecule type: mRNA
; A:Residues: 1-69, 'Q', 71-1014 <UCH>
; A:Cross-references: GB:M18112; NID:9190166; PIDN:AAA60137.1; PID:g190167
; R:Kurosaki, T.; Ushiro, H.; Mitsuuchi, Y.; Suzuki, S.; Matsuda, M.; Matsuda,
; Y.; Katunuma, N.; Kangawa, K.; Matsuo, H.; Hirose, T.; Inayama, S.; Shizuta, Y.
; J. Biol. Chem. 262, 15990-15997, 1987
; A:Title: Primary structure of human poly (ADP-ribose) synthetase as deduced
; from cDNA sequence.
; A:Reference number: A28498; MUID:88058958
; A:Accession: A28498
; A:Molecule type: mRNA
; A:Residues: 1-16, 'E', 18-211, 'K', 213-236, 'R', 238-366, 'H', 369-1014 <KUR>
; A:Cross-references: GB:J03473
; R:Cherney, B.W.; McBride, O.W.; Chen, D.; Alkhatib, H.; Bhatia, K.; Hensley,
; P.; Smulson, M.E.
; Proc. Natl. Acad. Sci. U.S.A. 84, 8370-8374, 1987
; A:Title: cDNA sequence, protein structure, and chromosomal location of the
; human gene for poly(ADP-ribose) polymerase.
; A:Reference number: A39976; MUID:88068596
; A:Accession: A39976
; A:Molecule type: mRNA
; A:Residues: 1-49, 'D', 51-612, 'Q', 614-907, 'Y', 909-939, 'R', 941-979, 'I', 981-1014
; <CHE>
; A:Cross-references: GB:J03030
; A:Note: the authors translated the codon ATA for residue 980 as Asn
; R:Suzuki, H.; Uchida, K.; Shima, H.; Sato, T.; Okamoto, T.; Kimura, T.; Miwa, M.
; Biochem. Biophys. Res. Commun. 146, 403-409, 1987
; A:Title: Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and
; expression of its gene during HL-60 cell differentiation.
; A:Reference number: A26901; MUID:87298455
; A:Accession: A26901
; A:Molecule type: mRNA
; A:Residues: 441-610, 'N', 612-880; 921-1014 <SUZ>
; A:Note: the sequence figure has an omission of forty residues
; R:Ogura, T.; Nyunoya, H.; Takahashi-Masutani, M.; Miwa, M.; Sugimura, T.;
; Esumi, H.
; Biochem. Biophys. Res. Commun. 167, 701-710, 1990
; A:Title: Characterization of a putative promoter region of the human
; poly(ADP-ribose) polymerase gene: structural similarity to that of the DNA
; polymerase beta gene.
; A:Reference number: I38096; MUID:90211250
; A:Accession: I38096
; A>Status: translation not shown
; A:Molecule type: DNA
; A:Residues: 1-40 <RES>
; A:Cross-references: EMBL:X16674; NID:g510112; PIDN:CAA34663.1; PID:g1017423
; R:Auer, B.; Nagl, U.; Herzog, H.; Schneider, R.; Schweiger, M.
; DNA 8, 575-580, 1989
; A:Title: Human nuclear NAD(+) ADP-ribosyltransferase (polymerizing):
; organization of the gene.
; A:Reference number: A33321; MUID:90091744
; A:Accession: B33321
; A:Molecule type: DNA
; A:Residues:
; 38-43; 93-98; 132-137; 204-209; 237-242; 276-281; 335-340; 384-389; 431-436; 512-517; 535-
; 540; 580-585; 645-650; 688-693; 716-721; 757-762; 800-805; 833-838; 884-889; 927-932; 947-
; 952; 986-991 <AUE>
; A:Cross-references: GB:M29544; GB:M22953
; A:Note: the authors translated the codon GTG for residue 54 as Glu
; A:Note: these fragments represent intron-exon boundaries
; A:Accession: A33321
; A>Status: nucleic acid sequence not shown; not compared with conceptual
; translation
; A:Molecule type: DNA
; A:Residues: 16-66; 96; 121-159, 'D', 161-167 <AUE>
; A:Note: these fragments represent a zinc finger-containing DNA-binding region
; R:Gradwohl, G.; Menissier de Murcia, J.; Molinete, M.; Simonin, F.; Koken, M.;
; Hoeijmakers, J.H.J.; de Murcia, G.
; Proc. Natl. Acad. Sci. U.S.A. 87, 2990-2994, 1990
; A:Title: The second zinc-finger domain of poly(ADP-ribose) polymerase
; determines specificity for single-stranded breaks in DNA.
; A:Reference number: A35635; MUID:90222155
; A:Accession: A35635
; A>Status: not compared with conceptual translation
; A:Molecule type: mRNA
; A:Residues: 12-26, 'T', 28-66; 116-166 <GRA>
; R:Schneider, R.; Auer, B.; Kuehne, C.; Herzog, H.; Klocker, H.; Burtischer,
; H.J.; Hirsch-Kauffmann, M.; Wintersberger, U.; Schweiger, M.
; Eur. J. Cell Biol. 44, 302-307, 1987
; A:Title: Isolation of a cDNA clone for human NAD (+): protein
; ADP-ribosyltransferase.
; A:Reference number: A61559; MUID:88082900
; A:Accession: A61559
; A:Molecule type: mRNA
; A:Residues: 381-420; 682-710 <SCH>
; R:Yokoyama, Y.; Kawamoto, T.; Mitsuuchi, Y.; Kurosaki, T.; Toda, K.; Ushiro,
; H.; Terashima, M.; Sumimoto, H.; Kuribayashi, I.; Yamamoto, Y.; Maeda, T.;
; Ikeda, H.; Sagara, Y.; Shizuta, Y.
; Eur. J. Biochem. 194, 521-526, 1990
; A:Title: Human poly(ADP-ribose) polymerase gene. Cloning of the promoter region.
; A:Reference number: S14010; MUID:91099327
; A:Accession: S14010
; A>Status: preliminary
; A:Molecule type: DNA
; A:Residues: 1-95 <YOK>
; A:Cross-references: EMBL:X56140; NID:g35286; PIDN:CAA39606.1; PID:g825702
; C:Comment: This protein can ADP-ribosylate itself as well as other proteins.
; C:Genetics:
; A:Gene: GDB:ADPRT; PPOL
; A:Cross-references: GDB:I19508; OMIM:173870
; A:Map position: 1q41-q42
; C:Superfamily: NAD+ ADP-ribosyltransferase
; C:Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus;
; pentosyltransferase; zinc finger
; A29725 Length: 1014 September 10, 2002 14:23 Type: P Check: 7353
; A29725
; MAESDILRYVEYAKSGRACCKCESIPKOSLRMAIMVQSPMFDGKVPWHVHFSFVKVGHSHRPOVE
; VDGSELRWDQOQVKYTAAGGVTKGQDGIKSKAEKTLGDFAAEYAKSNRSTCKGMEKIEKQVRLS
; KMDVDPQLGMDIDRWHPGCFVKNRRELGRPEYASQULGKFSLLATEDKEALKKOLPGVKSSEGRKG
; DEVGDPVAKKKSKDKLKAQNDLWNTKDELKVCSTNDLKEKLI FNKQVPSGSAIL
; DRADQWVFGALLPEECSGOLVPSKDAYCTGTAWTKCMVKTQTPNRKEWTPKFEISLYSLKLV
; KQDRIFPETSASVATPPSPASAAVSSADPLSNMKTLTLGKSRNKDEKAMTEKLGKLT
; TANAKASICTIKKEVKMKMEVEKANIRVYSEDFLDQVSASTKSLQELFLAHLILSPGAEVKAEPV
; EVAPRGSGAALSKSKGVKEGINSERKMLTLGKGAAYDPDSLEHSAHVLEKGGKVSATLGLV
; DIVKGTNYYKLQLEDKKNRYWIFRSGRVGTIGSKLEQMPKEDAEHFPMKLYEETKGNHWSKN
; FTKYPKFEYPLEIDYGODEEAVKLTVPNGTKSKLPKVPQDLIKMFVDSKMKAMVEYEDLQKMLPKG
; LSKQIQAAYSITLSEVQQAQSGSDSILDSNRYFTLIPHDFGKMPPLLNADSVQAKVEMLDLND
; LEVAYSLRGGSDSSKDPIDVNEKLTDKVVDRODSEAEIRKYVKNTHATNNAYDLEVIDFKIE
; REGCORYKPKQLHNRLLAHGSRFTNPFAGTISQGLRIAPPEAVTCYMGFGIYFADMYSKSNYCHT
; SQGDPGILILGEVALGNMYELKRAHSHSKLPKSKHVKSLGKLTTPDPSPANISLDGVDVPLGTGTGSSGVN
; DTSLLYNEYIYDIAQVNLKLLKLFNFKYSLMI

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; TOIG of: jh0581 check: 5006 from: 1 to: 1011
;
; P1: JH0581 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - chicken
; N: Alternate names: poly(ADP-ribose) synthase
; C: Species: Gallus gallus (chicken)
; C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
; C: Accession: JH0581
; R: Ittel, M.E.; Garnier, J.M.; Jeltsch, J.M.; Niedergang, C.P.
; Gene 102, 157-164, 1991
; A: Title: Chicken poly(ADP-ribose) synthetase: complete deduced amino acid
; sequence and comparison with mammalian enzyme sequences.
; A: Reference number: JH0581; MUID: 91340148
; A: Accession: JH0581
; A: Molecule type: mRNA
; A: Residues: 1-1011 <INT>
; A: Cross-references: EMBL:X52690; NID: g63742; PID: CAAG3691.1; PID: g63743
; C: Comment: This protein is a chromatin-bound enzyme.
; C: Comment: This enzyme catalyzes DNA-dependent post-translational modifications
; of various nuclear proteins.
; C: Superfamily: NAD+ ADP-ribosyltransferase
; C: Keywords: DNA binding; glycosyltransferase; NAD; nucleus;
; pentosyltransferase; zinc finger
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; JH0581 Length: 1011 September 10, 2002 14:23 Type: P Check: 5006
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; MAETGDKPYRAEYAKSGRASCCKGEGSIADKSLRLALMVOSPMFDGKVPWHHYSQFVKRAIVSHTDID
; GFPELRWEDQKIKKALETGALQEKGTREKVGKAEKSLTDFAAEYAKSNRSTCKCEQKIEKGQIRIS
; KKVHPPEKPOLGMDNHYHDFQSVSRAEQLFLPAYATQLLGSILKAEDKFLKKQLPATKEGRKRG
; EVDGNAVAKKSRKEKESQKQLEQTELIWIKDELKRVCSNDLKELLIANKEQVPSGENAILD
; RVADGMAFGALLPCECEKGFVFKSDAYYCGSDITAWTKCAKTQTPNRKDWIPKREIPYLLKFKCK
; KODRIFPEAATVNASPPASAPLTETVAPQDKPLTNMKILTGLKSNKEVKVNIIEELGCKMTTAA
; NKATLCISTQKEVKMSKMEVEKDAKRVVYSEFLDKVKSNNKFOELLSLHAI SPWGAEVKTEHOEVA
; VDGCSPANKKSAGKVEQGPSSKMKMLTVKGAAVDPDPSGLDSAHVPEKGGKIFSATLGLVDIV
; KGTNSYKLOLLEDDRESRYWVFSWGRVGTIGSNKLEOMPSEKEDAVEHNLNLYEKTGNSHRSKFTK
; YPKFYPEIDYGQDEAVKRLVSAGTKSLAKPIQDLNLMIFDVESKKAMVEFIDLOKMPGLKSLK
; QIOASYSILNEVQOAVDGGSESQILDLNRYFTLLPHDFGMKRPPLLNLEYIQARKVMDNLLDIEV
; AYSLLRGNEGDGDKDIDINYEKLRDIDKVVDDSEAKIKOYKVNTHAATHNAYDLKVEIFRIEREG
; ESQRYKPFQOLHNRLQHLHSGRTTNFAGILSQGLRIAPPEAPVTGYMGFGKIYPRDMVKSANYCHTSSQA
; DPGLILLIGEVALGNMYELKNASHITKLPKGVKSLGKGTAPDPTATTTLDDGVEVPLNGISTGINDTC
; LLYNEYIYDYVAQVNLAYLLKLFNKYKTSLW1
;
; JH05428 Length: 1016 September 10, 2002 14:13 Type: P Check: 8204
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; MAESSDKLYRVEYAKSGRASCCKKESIPKDSIRMAFVSPMFDGKIPHWIHLSCFWKVFSTIWHPDVE
; VEGFSELRWDDQOTIKKMAETGGRTDVGKGVGSGKTEKTLIDFGAGYAKSNRSTCKSCMEKIDKGOV
; RLKSKVVPDQKPOLGMDNHYHDFQSVSRAEQLFLPAYATQLLGSILKAEDKFLKKQLPATKEGRK
; RKGDEVDGIDEVYKKSKKEKDEIKLEKALKAQNDLIWNVKDELKACSTNDLKELLIENKQVPSGES
; AILDRVADGMVFGALLPCEECGQLVFKGDAYTCTGDTATWTKMVKITQTPNRKEWVTPKREIFSTFKK
; LKTKQDRIFPPESSTPVGAAPPASAAAPVHSPPDRPLSNMKILTGLKLSQNKDEKVRATIEKILGGK
; LTGTANKASLCISTKKEVDKLNKMEVEKANI RVSEDFLODTSASTKLOELLSTHLISPMWGAEVKE
; PVEAVGPKGSGAAPS KSKSGPKVEGTNKSEKRMKLT LKGGAAVDPDPSGLDHNHLEKGGKVFSATLG
; LVDIVKGTNSYKLOLLEDDKESRYWIFRSKGRVGTIGSNKLEOMPSEKEDATIEHFMKLYEETGNWHS
; KNTTKHPKRYPLEIDYGQDEAVKLTVPNGTKSLKLPQVNLKIMFDVESKKAMVEFIDLOKMP
; GLSKRQIQAYISILSEVQOALSGQSDSHILDLSNRYFTLLPHDFGMKRPPLLNANSVOAKVEIDLNL
; LDIEAVYSLRGSDSDSKDPIDVNEKLRDIDKVVDDSEAEIIRKYKVNTHAATHNAYDLEVDIFK
; IERESORYLKPFQOLHNRLHWSGRTTNFAGILSGLRIAPPEAPVTGYMGFGKIYFADWVKSANYC
; HTSQGDDPGLILLIGEVALGNMYELKHARHISKLPKGVKSLGKGTTPDPSASITVDGVEVPLGTGISSG
; VNTCLLYNEYIYDYVAQVNLAYLLKLFNKYKTSLW1
;
; JH05428 Length: 1016 September 10, 2002 14:13 Type: P Check: 8204
;
; MAESSDKLYRVEYAKSGRASCCKKESIPKDSIRMAFVSPMFDGKIPHWIHLSCFWKVFSTIWHPDVE
; VEGFSELRWDDQOTIKKMAETGGRTDVGKGVGSGKTEKTLIDFGAGYAKSNRSTCKSCMEKIDKGOV
; RLKSKVVPDQKPOLGMDNHYHDFQSVSRAEQLFLPAYATQLLGSILKAEDKFLKKQLPATKEGRK
; RKGDEVDGIDEVYKKSKKEKDEIKLEKALKAQNDLIWNVKDELKACSTNDLKELLIENKQVPSGES
; AILDRVADGMVFGALLPCEECGQLVFKGDAYTCTGDTATWTKMVKITQTPNRKEWVTPKREIFSTFKK
; LKTKQDRIFPPESSTPVGAAPPASAAAPVHSPPDRPLSNMKILTGLKLSQNKDEKVRATIEKILGGK
; LTGTANKASLCISTKKEVDKLNKMEVEKANI RVSEDFLODTSASTKLOELLSTHLISPMWGAEVKE
; PVEAVGPKGSGAAPS KSKSGPKVEGTNKSEKRMKLT LKGGAAVDPDPSGLDHNHLEKGGKVFSATLG
; LVDIVKGTNSYKLOLLEDDKESRYWIFRSKGRVGTIGSNKLEOMPSEKEDATIEHFMKLYEETGNWHS
; KNTTKHPKRYPLEIDYGQDEAVKLTVPNGTKSLKLPQVNLKIMFDVESKKAMVEFIDLOKMP
; GLSKRQIQAYISILSEVQOALSGQSDSHILDLSNRYFTLLPHDFGMKRPPLLNANSVOAKVEIDLNL
; LDIEAVYSLRGSDSDSKDPIDVNEKLRDIDKVVDDSEAEIIRKYKVNTHAATHNAYDLEVDIFK
; IERESORYLKPFQOLHNRLHWSGRTTNFAGILSGLRIAPPEAPVTGYMGFGKIYFADWVKSANYC
; HTSQGDDPGLILLIGEVALGNMYELKHARHISKLPKGVKSLGKGTTPDPSASITVDGVEVPLGTGISSG
; VNTCLLYNEYIYDYVAQVNLAYLLKLFNKYKTSLW1
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TOIG of: s26057 check: 8491 from: 1 to: 500

F1:S26057 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 18-Jun-1999

C:Accession: S26057; S78453; I52331

R:Thibodeau, J.; Gradwohl, G.; Dumas, C.; Clairoux-Moreau, S.; Brunet, G.; Penning, C.; Poirier, G.G.; Moreau, P.

Biochem. Cell Biol. 67, 653-660, 1989

A:Title: Cloning of rodent cDNA encoding the poly(ADP-ribose) polymerase catalytic domain and analysis of mRNA levels during the cell cycle.

A:Reference number: I52331; MUID:90027702

A:Accession: S26057

A:Molecule type: mRNA

A:Residues: 1-500 <THI>

A:Cross-references: EMBL:X65497; NID:g56849; PIDN:CAA46478.1; PID:g56850

R:Potvin, F.

submitted to the EMBL Data Library, March 1992

A:Reference number: S78453

A:Accession: S78453

A:Molecule type: mRNA

A:Residues: 1-124, 'H', 126-127, 'A', 129-238, 'D', 240-500 <POF>

A:Cross-references: EMBL:X65497

C:Superfamily: NAD+ ADP-ribosyltransferase

C:Keywords: DNA binding; DNA repair; glycosyltransferase; NAD; nucleus; pentosyltransferase

S26057 Length: 500 September 10, 2002 14:23 Type: P Check: 8491

GVNKSERKMKLTLLKGAADVDPDSGLSHSAHVLEKGGKVFSAITGLVDIVKGTNSYKQLQLESDESRVW

IFRSWGRVGTVIGSNKLEQMPKEDAVEHPMKLYEKTGNWHSKNFTKPKFPYPLEIDYGODEAVKK

LAVKPGTKSLPKPVQELVCMIFDVESMKALVEYEDLQKMPGLKSLRQIQOAYSILSEVQOAVSQGS

SESQLDLSNRFYTLPHDFGKKPPLNNNTDSVQAKVEMLDNLDIEVAILRGSDSSSKDPIDVNY

EUKTIDIKVVDROSEAEVIRKVKNTATHNAYDLEVIDIFKIEREGESQRYKPPRQLHNRLLWHGS

RTTNFAGILSQGLRIAPPEAPVTGYMGKGIYPADVMKVSANTYCHTSQGDPIGLILILGEVALGNMYELKH

ASHISKLPGKHSVKGGLGTAPDPSASITLDGVEVPLGTGIPSGVNDTCLLYNEYIIVYDIAQVNLKYLK

LKFNFTSLW1

TOIG of: s31735 check: 6153 from: 1 to: 998

F1:S31735 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - African clawed frog (fragment)

N:Alternate names: poly ADP-ribose polymerase

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C:Accession: S31735; PN0495

R:Saulier-le Dreal, B.M.

submitted to the EMBL Data Library, May 1992

A:Reference number: S31735

A:Accession: S31735

A:Molecule type: mRNA

A:Residues: 1-998 <SAU>

A:Cross-references: EMBL:Z12139; NID:g64967; PIDN:CAA78126.1; PID:g1334661

R:Ozawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.

Biochem. Biophys. Res. Commun. 193, 119-125, 1993

A:Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose)polymerase from xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences.

A:Reference number: PN0494; MUID:93277538

A:Accession: PN0495

A:Molecule type: mRNA

A:Residues: 742-745, 'E', 747-876 <OZA>

C:Superfamily: NAD+ ADP-ribosyltransferase

C:Keywords: DNA binding; glycosyltransferase; hexosyltransferase; NAD; nucleus; pentosyltransferase; zinc finger

S31735 Length: 998 September 10, 2002 14:22 Type: P Check: 6153

AKSGRACKKCGDNIAKESLGLAIMVQSPMFDGKVPWHHYSFCWKRARVLSQGGDIYGYTELWEDQEMI

KKAIETGGAAGAGDSKGGKEMTLNDFAAEYAKSNRSACKGCEQKIEKQIRISKSVDPVLPQIGMI

DRYHPDCVFSREEDFLPSYASQLKGTILISAEDKSLKKLPVKNKGRKADVDGHSAAATKKKI

KKEKESKLEKLLKEQTELIWHIKDELKVKCSTNDLKIANKQOVPSGETNIVDRVSDGMAGFALLP

CECSGQVFKGDAYCTGDSAWTKCAVKTQPNRKDWTPKEFHEIPYLKFKRHRARPPCAAPT

PISPRAAPEKPTVEETFPSEKPLTNTKLLIGLKNKDEVTLEIGLQKGVAGSAKHNLCISTNKEV

KMSKMEEVKAANRVVSDDFLKEVESGKSVQELLQSFGISWGAIEKQENAVQTEKQSPSPVAGKSS

GVYKEEKGSNKSEKMKLTVKGGAADPDSLEDSCHVLTGGKIFSATLGLVDITRGTNSYKQLQIEH

DRDSRYWFRSGRVGTVIGSKLEEMSKEDAIEHFLNLYQDKTGNWHSKNFTKPKFPYPLEIDYGQ

EEDVVKLSVAGTKSKLAPVQELIKLIFDVESMKKAMVEFEDLQKMPGLKSRQIQOAYSILSQVQ

QAVSELSSEARLLDLSNOFTLIPHDFGKKPPLNNLEYIOAKVQMLDNLDEYVAILRGADGEX

DPIDVAYEIKTDIKVVKADSESRILICDVKNTHADTHAYDLEVIDIEFKIDREGEVQRYKPKQLHNR

QLLWHSRTTNFAGILSQGLRIAPPEAPVTGYMGKGIYPADVMKVSANTYCHAMPSPGILGILLGEVALG

NMHELKAASQITKLPKGSVKVKGGLGTAPDPSATVQLDGVDVPLUGKTSANISDTSLLINEYIIVYDIAQV

NLKYLLKLFKNYKGGMMW1

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; TOIG of: s42208 check: 1061 from: 1 to: 996
;
; P1:S42208 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - flesh fly (Sarcophaga
; peregrina)
; N:Alternate names: poly(ADP-ribose) polymerase
; C:Species: Sarcophaga peregrina
; C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
; C:Accession: S42208; S71496
; R:Masutani, M.; Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki, K.; de Prati,
; A.C.; Kurata, S.; Natori, S.; Sugimura, T.; Esumi, H.
; Eur. J. Biochem. 220, 607-614, 1994
; A:Title: Cloning and functional expression of poly(ADP-ribose) polymerase cDNA
; from Sarcophaga peregrina.
; A:Reference number: S42208; MUID:94170813
; A:Accession: S42208
; A:Molecule type: mRNA
; A:Residues: 1-996 <MAS>
; A:Cross-references: EMBL:D16482; NID:g473742; PIDN:BAA03943.1; PID:g538248
; A:Accession: S71496
; A:Molecule type: protein
; A:Residues: 170-188; 721-736; 813-819; 879-885 <MAX>
; C:Superfamily: NAD+ ADP-ribosyltransferase
; C:Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc
; finger
; F:1-369/Domain: DNA binding #status predicted <DNA>
; F:370-507/Domain: auto-modification #status predicted <AMO>
; F:508-996/Domain: NAD binding #status predicted <NAD>
;
; S42208 Length: 996 September 10, 2002 14:23 Type: P Check: 1061
S42208
MEIDLPLFKVEYSKSRASCKGNKIEAGILRIAAMVQSAFHDGKQPNWFHQCFQKQRPPTSAGDIENF
ENIRFEDQRIKKAIDNCTTVISAGSGKAKRSKGNNAIKDFGIEYAKSGRCGCEQRIKDKQIRI
RKTVPDETVGMVGGPQIWHVHVECPAOLGELGLDGTGNLPGFOTLKSDDKADYKKALPVIKDEGVSA
KKAKLEKIDEDAAASKELTEKIKQSKRLFRFEIKNEMSKDWMVALLENMPEYKGDSEKLLDQVA
DLITFALLPCITDCGRQLLHFHSGTLCNGDLUTWTCKTLKEPERKSKIPGVLKYKFLKADVRKNPEV
RAIRYIPPTSTILKNISLKGDGLDGPVKVRPPLYNIEIALIPKEREIVKDRISKLGGTVSTKIT
ERTVVLSTPEEVERSMRSMKAKTGLHVIPEDEYLAVEQNGAGAINYISSMLCDMGTDPATRITQBE
SKSSKSKIYTKSVKSWTLKITDGLVADPDSGLDEVAHVYVRNKEKYNVVLGITDQKNKNSFYKLQI
LESDMKNRFPVRSRGRICTTIGGNLDNFSNLVDALVQFKELYLEKSCNHFENRENVKVGAWVPIDI
DYAEDSKIDLSAEHDKSKLPLSVQDILKLMFVDSMKRTMWFEDLMEKHPGLKLSQKIQISAYKVLTE
DINPIDKHVEQLTKLEPLDKNSEEYILQKYVKNTHAETHKLYDLEVVDIFPKVARQGEARRYKPFKLH
NRLLWHGSRLLTFAILSHGLKIIAPPEAPVTGYMFGGIYFADVMVRSANYCCTSHHNSTGLMLLSEVA
LGMNMECTAAKYVTKLPNDKHSCFCGRGRTMPNPSEIREDGVEIPLGKPIITNDSLKSLLYNEFIIVDI
AQVNIQYMLRMNEFKYKI
```

```
; TOIG of: t01311 check: 5648 from: 1 to: 635
;
; P1:T01311 - NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - Arabidopsis thaliana
; N:Alternate names: poly(ADP-ribose) polymerase; protein T14P8.19
; C:Species: Arabidopsis thaliana (mouse-ear cress)
; C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
; C:Accession: T01311; S65662
; R:Kalicki, J.; Elliott, G.; Cloud, J.
; submitted to the EMBL Data Library, May 1998
; A:Description: The sequence of A. thaliana T14P8.
; A:Reference number: Z14290
; A:Accession: T01311
; A>Status: translated from GB/EMBL/DBJ
; A:Molecule type: DNA
; A:Residues: 1-635 <KAL>
; A:Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193299
; A:Experimental source: cultivar Columbia
; R:Lepiniec, L.; Babychuk, E.; Kushnir, S.; Van Montagu, M.; Inze, D.
; FEBS Lett. 364, 103-108, 1995
; A:Title: Characterization of an Arabidopsis thaliana cDNA homologue to animal
; poly(ADP-ribose) polymerase.
; A:Reference number: S65662; MUID:95269779
; A:Accession: S65662
; A>Status: nucleic acid sequence not shown
; A:Molecule type: mRNA
; A:Residues: 1-115; 'GT', 116-635 <LEP>
; A:Cross-references: EMBL:248243; NID:g853721; PIDN:CAA88288.1; PID:g853722
; C:Genetics:
; A:Gene: PARP
; A:Map position: 4
; A:Introns: 28/3; 116/1; 162/3; 190/1; 268/3; 312/1; 330/3; 355/2; 371/1; 387/3;
; 408/3; 435/3; 472/3; 498/1; 545/3; 570/2; 605/3
; A:Note: T14P8.19
; C:Keywords: DNA binding; glycosyltransferase; NAD; pentosyltransferase; zinc
; finger
;
; T01311 Length: 635 September 10, 2002 14:13 Type: P Check: 5648
t01311
MANKLVDELRLKLAERGLSTGVKAVLVERLEEAIADTKKEESKSKRKNSSNDTVESNKLIAIGFER
GMIVKELREAIKRGDITGTIKDLELRCDANNVSNAPVKSNDDEADDNNGFEERKEKIVTATKK
GAALVDQIPDIEIKSOYHVLQRDQDDVAILNQTNRNNKFFVLQLESDSKKTYVYTWIRGVGVKG
QSKLGPYDSDWRAIEITFNKNDKTYNSDRKEIPIPHKSYTWLEMDYKGEENDSPVNNNDIPSSSEV
KPEQSKLDRVAKFTSLICNYSMAQHMEIGYNANKPLGKISKTSKGYEVLKRISSEVIDRDRTRL
BELSGEFTVIPHDFGFKKMSOFVITDTPQKQKTEMVEALGEIELATKLLSVDPGLQDDPLLYHYHQLN
CGLTVPQNDSEESFSAVNYMTHAKTHSGYTVETIAQLFRASRAVEADRFQOFSSKKNMMLLHWSRLTN
WAGILSQGLRTAPPEAPVTGYMFGKGVTFADMFSAKSNCTANTGANDGVLLICEVALGDMNELLYSDYN
ADNLPPKGLSTKRGVKGKTAQTNLEDDGVVVVPLGKPVRSCKSMGLLYNEYIVINVEQIKMRYIOVK
FNKHI
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! FINDPATTERNS on *.pir* allowing 0 mismatches
!      1 CXXCX{28,30}HXXC      September 10, 2002 14:25 ..

a29725.pir1 ck: 7353 len: 1.014 ! P1:A29725 - NAD+ ADP-ribosyltransferase (EC
1      CXXCX{28,30}HXXC
      CXXCX{28}HxxC
21: SGRAS CKKSESIIPKDSLRLALMVQSPMFDGKVPWHYHFS FVKVG
125: SNRST CKGCMEXIEKQVRLSKMVDPEKPOLGMIDRWYHPG FVKNR

jh0581.pir1 ck: 5006 len: 1.011 ! P1:JH0581 - NAD+ ADP-ribosyltransferase (EC
1      CXXCX{28,30}HXXC
      CXXCX{28}HxxC
21: SGRAS CKKGESIAKDSLRLALMVQSPMFDGKVPWHHHYSC FWKRA
125: SNRST CKGCEQIEKQIRISKWVHPEKPOLGMIDNWIHPDC FVSRR

js0428.pir1 ck: 8204 len: 1.016 ! P1:JS0428 - NAD+ ADP-ribosyltransferase (EC
1      CXXCX{28,30}HXXC
      CXXCX{28}HxxC
21: SGRAS CKKCESIPKDSIRMAFVESPMDGKIPWHYHLSC FWKVG
128: SNRST CKSCMEKIDKQVRLSKKVYPDKPOLGMVDCWYHPKC FVQKR

s31735.pir2 ck: 6153 len: 998 ! F1:S31735 - NAD+ ADP-ribosyltransferase (EC
1      CXXCX{28,30}HXXC
      CXXCX{28}HxxC
8: SGRAS CKKCGDNIAKESLGLAIMVQSPMFDGKVPWHHHYSC FWKRA
111: SNRSA CKGCEQIEKQIRISKSDVERPOLGMIDRWYHPDC FVSSR

s42208.pir1 ck: 1061 len: 996 ! P1:S42208 - NAD+ ADP-ribosyltransferase (EC
1      CXXCX{28,30}HXXC
      CXXCX{28}HxxC
19: SSRAS CKGCKNIEAGILRIAAMVQSAFHDGKQPNWFHEQC FFQKQ
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Total finds: 9
Total length: 6,170
Total sequences: 7
CPU time: 00.04

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TOIG of: aar99642 check: 3219 from: 1 to: 1013

ID AAR99642 standard; Protein; 1013 AA.

AC AAR99642;

XX

DT 31-OCT-1996 (first entry)

XX

DE Poly(ADP-ribose) polymerase contg. DNA-binding domain.

XX

KW PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;

KW tumour treatment; DNA repair; over-expression.

XX

OS Homo sapiens.

XX

PN W05618737-A2.

XX

PD 20-JUN-1996.

XX

PF 15-DEC-1995; 95WO-DE01817.

XX

PR 16-DEC-1994; 94DE-4444949.

XX

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX

PI Buerkle A, Kuepper J, Zur Hausen H;

XX

DR WPI: 1996-300654/30.

DR N-PSDB; AAT13732.

XX

PT Vectors contg. insert encoding DNA-binding domain of

PT poly(ADP-ribose) polymerase - useful for gene therapy, esp. of

PT tumours

XX

PS Disclosure; Fig 1; 22pp; German.

XX

CC The present sequence is that of a poly(ADP-ribose) polymerase (PARP)

CC contg. a DNA-binding domain (DBD). It is encoded by AAT13732, from

CC which a fragment comprising nucleotides 67-1220 (-29 to +1127) encoding

CC the DBD can be inserted into vectors which are used for gene therapy.

CC Over-expression of the DBD inhibits the DNA repair function of PARP, so

CC the vectors are useful for gene therapy or tumours, esp. in combination

CC with conventional chemo- and/or radiotherapy.

XX

SQ Sequence 1013 AA;

AA99642 Length: 1013 September 10, 2002 14:39 Type: P Check: 3219

MAESSDKLYRYEAKSERACKSCSEIPKDSLRMAIMVQSPMFGKVPWHYHFCFWKVGHSIRHPDVE

VDFSELRWDQQRKATAGAGTGQDGIGSKAEKTLGDFAAEYAKNRSTCKGCMKIEKGQVRLS

KMWDPKPOLGMDIRWYHGPCVKNREELGFRPEYSASOLKGFSLLATKQKALQKLPVKGSEGRKG

KVDGVDEAKKSKKEDKDKSLKELKQNDLNNIKRDELKVKVSTNDLKELLIFNKQOVPSGSAIL

DRVADGMVGFALLPCSECSQVFKSDAYCTGDTAWTKCMVKTPTPNKRWTPREFREISYLKLLAV

KQDRIFPPTASVAHPPTASAPAAVNSASADKPLSNMKILTLGLSRNKNDEKAMIELGKGLTG

TANKSLICTTKEVEKMMKMBEVEKANI RVVSEDFLOVYASTKSLQELFLAHLISPMGAEVKAEPVE

VVAPRGSGAALSQKGVKEGINKSEKRMKLTLLGGAAVDPDSGLEHSAHLKGGKVFSAITGLVD

IVKTNYSYKLOLDDKNRYWIFRSWGRVTVIGSNLEOMPSKEDATEHFMKLYEERTGNAMHSKNF

TKYPKFPYPLEIDYGDEEAVKLTVPNCTKSLPKPVODLKIPIEDVESMKKAMVEYEDLQKPLGKL

SKQIQNAVLSILEVQAVSQSSDQLDLSNRFYTLPHDFGMRKPPLLNNADSVQARVEMDLNLLDI

EVAISLLRGSSDSSKDDIDVNTYKLUKTDIKVDVDRDSEAEAIRKYVKNTHATTHAYDLVIDIFKIER

EGECQRYKPKPOLHNRRLNRLNFGILSQGLRIAPPEAPVTGYMFGKIYFADMYSKSANTCHTS

QGDPILGILGELVALGNMYELKHAHSIKLPKGRKHSVKGIGKTTDPSPANSISLDGVDVPLGTGTSISVND

TSLLYNEYIVDYIAQVNLKYLKLFNFKTSLW1

TOIG of: aay68834 check: 7074 from: 1 to: 653

ID AAY68834 standard; Protein; 653 AA.

XX

AC AAY68834;

XX

DT 16-MAY-2000 (first entry)

XX

DE A poly(ADP-ribose) polymerase NAP protein of Zea mays.

XX

KW NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;

KW programmed cell death; apoptosis; growth rate; stress; cold; pathogen;

XX

OS pest; drought; heat; fungi; nematode; seed-shatter.

XX

PN Zea mays.

XX

PD

XX

PF Key Location/Qualifiers

XX Misc-difference 1..159

FT /note= "these residues are specifically claimed in

ET Claim 18"

XX

PN W0200004173-Al.

XX

PD 27-JAN-2000.

XX

PF 12-JUL-1999; 99WO-EP04940.

XX

PR 17-JUL-1998; 98US-0118276.

XX

PA (PLBZ) PLANT GENETIC SYSTEMS NV.

XX

PI Babychuk E, Kushnir S, De Block M;

XX

DR WPI: 2000-182436/16.

DR N-PSDB; AAZ60616.

XX

PT Modulating cell death, growth and stress resistance in eukaryotes,

PT specifically plants, used, e.g. to impart fungus or nematode resistance

XX

PS Claim 18; Page 92-95; 126pp; English.

XX

CC The present sequence represents the NAP protein of Zea mays. This

CC protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as

CC poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed

CC cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide

CC sequences can be used for modulation of programmed cell death in

CC eukaryotic cells. The method is used, specifically in plants, to induce,

CC or protect against, programmed cell death, depending on the extent to

CC which PARP activity is reduced. Reducing expression of endogenous NAP

CC class PARP only is also used to modulate programmed cell death, to

CC increase growth rate and to produce plant cells that are more tolerant

CC of stress (cold, chemical treatments, pathogens, pests, drought, heat,

CC etc., or during transformation). Particular applications are generation

CC of plants that are resistant to fungi or nematodes; are male or female

CC sterile; or have better seed-shatter properties. The methods are also

CC used to improve growth of transformed plant cells (and derived calli or

CC complete plants).

XX

SQ Sequence 653 AA;

AA68834 Length: 653 September 10, 2002 14:38 Type: P Check: 7074

MSARLRVADVRAEQLQRGLDVSGTKPALVRRLLDAACEAKAVVAAPTSAVANGVAVDGRKNCGNKR

KRSGDGGEEGNDTCTDVTKLEGSYRELQGLAKARGVAANGKKDVIOQLLSATAGPAVADGGPLGAK

EVIKGGDEEVKKERKMTATKGAVALDQHI PDHIVLQVGDIEYDNLQNTVGDNNNNFYIIO

VLESDAGGSPMYNRWGRVGRQDGLHGSPTRDQAIYEFEGKFNKTNHNSDRKNFCYAKKVTWLE

MDYGETEKETEGSITDOLKETLETRIAOFISLIGNISNMKORMVEIGYNAEKLPLGKLRKATILKGYH

VKRI SDVTSKADRRHLEQLTGFTYVIPHDFGRKMRFIIDTPQKLKAKLENVEALGEGIEATKLLD

DSSDQDDPLYARKQLHCDFTPLEADSDSEYMSIKSLRNTHKTHSGTYVDI VOIFPKYSRHGETERQKF

ASTRNMLLHWGSRLSNAGILSQGLRIAPPEAPVTGYMFGKIYFADMYSKSANTCHTS

CEVALGDMNELLNADYDANNLPKGLRKSQGVGTAPNWNVESKVADGCVVYVPLGPKQEPSKRGGLLYNEY

IVYNVDQIRRMRYVLHVNFNFKRR1

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! FINDPATTERNS on *.geneseq* allowing 0 mismatches
1      1 CXXCX[28,30]HXXC      September 10, 2002 14:41 ..
aar99642.geneseqp1990s ck: 3219 len: 1,013 ! ID  AAR99642 standard; Protein; 1013 AA
1      CXXCX[28,30]HXXC
      CXXCX[28]HxxC
21: SERAS CKKCESEIPKDSLRMAIMVQSPFMFDGKVPDHWYHFSC FWKVG
      CxxCx[30]HxxC
125: SNRST CKGCMKIEKGQRLSKKMDPEKPOLGMIDRWYHPGC FVKNR

Total finds:      2
Total length:    1,666
Total sequences: 2
CPU time:        00.02
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